SUPPLEMENT

Genetic methods for identifying baffin bay polar bears

The analysis of individual identity followed a 3-phase approach. Phase 1 was a first pass of all extracted samples using the 9 selected markers (microsatellites *G10B, CXX20, G10H, G10P, 145P07, MU50, MU59* and *G10X*, plus a *ZFX*/*ZFY* sex marker). These markers were selected for high variability in the study population, with the mean observed heterozygosity of the 8 microsatellite markers being 0.81 in the 1223 individuals genotyped in this project. Primer sequences and PCR conditions were as described by Paetkau et al. (1998), except that amplification was performed on MJ Research PTC-100 thermal cyclers and PCR products were resolved on Applied Biosystems 310 and 3130XL genetic analyzers.

Samples that failed at > 6 of 9 markers on the first pass were set aside and did not proceed further in the analyses. Such samples are prone to errors and generally run out of DNA before generating a complete (phase 2) and reproducible (phase 3) genotype (Paetkau 2003).

The first pass was followed by a cleanup phase in which data points that were weak or difficult to read the first time were re-analyzed. During cleanup we used 5 µL of DNA per reaction instead of the 3 µL was used during first pass. At the conclusion of the cleanup phase, the remaining samples (99.5%) had high-confidence scores for all 9 markers. In cases where the genetic sex result contradicted the reported sex based on field assessment, genetic sex was checked using a second independent marker (*amelogenin*; http://www.ncbi.nlm.nih.gov/pubmed/7695123), thus confirming the results, and ruling out the possibility that a mutation at a particular marker was to blame. In all cases, results from the second marker confirmed that the field data was the source of error.

The third and final phase of analysis was error-checking, following the published protocol of reanalyzing the mismatching markers in highly similar pairs of genotypes (Paetkau 2003). This error-check included genotypes from the 4,657 polar bears in the database, plus published data from 473 individuals (Paetkau et al. 1999). The error-checking protocol functions on the principle that when ≥ 2 samples are genotyped from a given individual, and when 1 of those genotypes contains an error, the result is a pair of genotypes that match at all-but-1 marker (a '1MMpair'). Less commonly, 2MM-pairs are created when 2 errors have been made in the genotypes of the samples from a given individual.

An important distinction with this protocol is that it is designed to ensure accurate individual ID and has been proven to do so with a high degree of efficiency (Kendall et al. 2009), but it is not intended or expected to correct errors when just 1 sample has been genotyped from a given individual. In addition to re-analyzing mismatching markers this protocol also involved the inclusion of additional markers for some samples.

In addition to the genotyping errors that were targeted during error-checking, DNA-based datasets are prone to a second source of error, when match probabilities are so high that some individuals have identical genotypes. Calculated match probabilities provide no practical insight into the risk of sampling individuals with matching genotypes, because the calculations are so dependent on the assumptions made about the degree of relatedness among the sampled individuals. We therefore used the direct, empirical approach of extrapolation from the observed mismatch curve (Fig. S1). We expect to see roughly order-of-magnitude decreases in the number of pairs of individuals whose genotypes match at increasing numbers of markers

(Paetkau 2003). In our dataset the slope of this curve was reasonably true to that rule of thumb. From this curve, it is estimated that we would have sampled ~ 0.3 0MM-pairs (individuals whose genotypes matched at 9 markers) in this multiyear dataset of 4,657 individuals; a very small risk of error in proportion to the size of the dataset. In addition to reducing the risk of sampling individuals with the same genotype, another benefit to having such a powerful marker system was realized during error-checking, where the amount of time required to reanalyze the mismatching markers underlying 1MM- and 2MM pairs was trivial in proportion to the scale of the project, because there were so few such pairs. The single pair of individuals with genotypes that match at 8 of 9 markers ('1MM-pair') comprises cubs of the year sampled at the same time and place [bb-2012-302 & 303]. This illustrates the principle that siblings are more likely to have identical genotypes than unrelated individuals (Woods et al. 1999).

LITERATURE CITED

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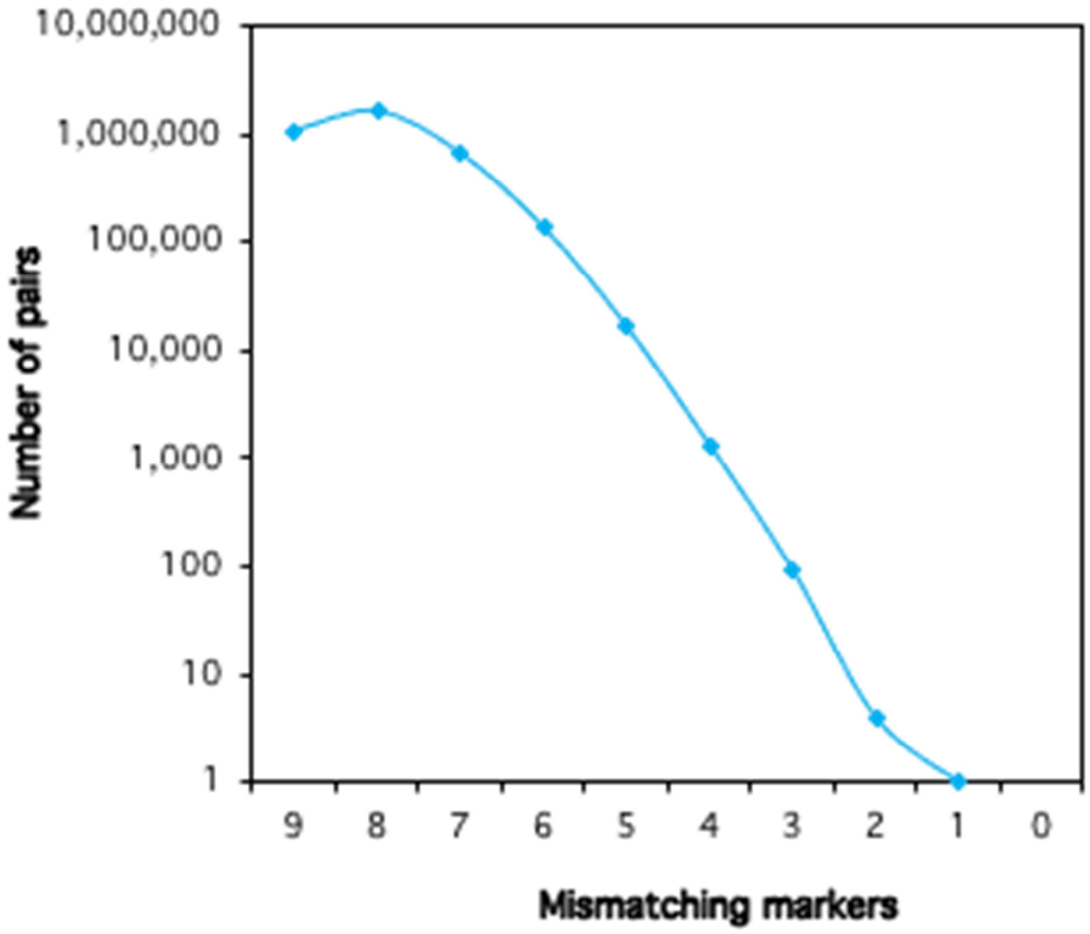

Fig. S1. Nine-locus mismatch distribution for 2,637 polar bears with genotypes for all 9 loci that were either included in our analysis, or that had been sampled in the Baffin Bay zone in the 1990s or 2000s and were not known to be dead prior to 2011. The 2,637 polar bears included all bears sampled by capture or biopsy between 2011-201, all bears that were sampled by capture in the 1990s that were not known to have been harvested or died before 2011, and all bears that were harvested in BB or neighboring subpopulations between 2011 and 2013. Unlike calculated match probabilities that require a level of relatedness to be assumed (e.g. sibling match probability), the distribution of degrees of relatedness among the study animals is implicit in the mismatch curve. Empirical testing with datasets of known individuals confirms that extrapolation from a mismatch curve provides a practical estimate of the number of pairs of individuals in the dataset with identical genotypes ('0MM-pairs'). With 4 2MM-pairs and 1 1MM-pairs among these 2,637 bears, extrapolation predicts that the most likely number of false matches is 0 (i.e. that we were able to generate a unique 9-locus genotype for every individual sampled).

Table S1. Survival sub-model structures evaluated in mark-recapture analysis of the Baffin Bay polar bear subpopulation data, 1994–2013

S sub-model	Age[a]	Sex	Temporal[b]	Environmental
1	2 class	Age 2+ only	Constant	None
2	2 class	Age 2+ only	3 epoch + sex	None
3	2 class	Age 2+ only	3 epoch × sex	None
4	2 class	Age 2+ only	Constant	Ice transition
5	2 class	Age 2+ only	Constant	Ice area
6	3 class	Age 2+ only	Constant	None
7	3 class	Age 2+ only	3 epoch + sex	None
8	3 class	Age 2+ only	3 epoch × sex	None
9	3 class	Age 2+ only	Constant	Ice transition
10	3 class	Age 2+ only	Constant	Ice area

[a]2 class: cub-of-year (COY) plus yearling (1) vs. subadults plus adults (2+); 3 class: COY vs. yearling vs. Age 2+

[b]3 epoch: 1994–1997, 1998–2010, vs. 2011–2013

Table S2. Recapture probability sub-model structures evaluated in mark-recapture analysis of the Baffin Bay polar bear subpopulation. All models included a Radio covariate for bears that were outfitted with a satellite collar that may have been used to locate individuals for recapture. Bears that were not genotyped were unavailable to be recaptured during the 2011–2013 sampling window, so p was fixed to 0 for non-genotyped bears

p sub-model	Family	Temporal	Geographic	Ice
1	Yes	2 epoch + family	None	None
2	Yes	2 epoch + family	Coastline, 2 epoch	None
3	Yes	2 epoch + family	Coastline, 2010s	None
4	Yes	2 epoch + family	None	Spring
5	Yes	2 epoch + family	Coastline, 2 epoch	Spring
6	Yes	2 epoch + family	Coastline, 2010s	Spring
7	Yes	2 epoch × family	None	None
8	Yes	2 epoch × family	Coastline, 2 epoch	None
9	Yes	2 epoch × family	Coastline, 2010s	None
10	Yes	Annual + family	None	None
11	Yes	Annual + family	Coastline, 2 epoch	None
12	Yes	Annual + family	Coastline, 2010s	None

Table S3. Summary table of live captures and dead recoveries during the mark-recapture study of the Baffin Bay polar bear subpopulation in Nunavut, Canada, and Greenland, 1993–2013. Shaded cells indicate that data are non-existent due to an absence of marking or recapture

	Initial captures						**Live recaptures**				**Dead recoveries**					
	Females			Males			Females		Males		Females			Males		
Year	**COY**	**YRL**	**2+**	**COY**	**YRL**	**2+**	**YRL**	**2+**	**YRL**	**2+**	**COY**	**YRL**	**2+**	**COY**	**YRL**	**2+**
1993	14	8	53	12	8	61					0	0	1	0	0	0
1994	26	13	65	16	9	77	0	5	0	14	0	0	3	0	0	7
1995	15	11	62	19	11	85	4	11	4	23	0	2	6	1	0	8
1996												1	8		0	7
1997	22	10	60	19	13	113		20		31	0	0	6	0	1	9
1998												0	3		0	11
1999													3			9
2000													0			8
2001													2			8
2002													0			11
2003													0			7
2004													1			7
2005													2			3
2006													3			6
2007													1			2
2008													2			4
2009													2			0
2010													0			1
2011	2	23	163	1	20	148		5		5	0	0	4	0	0	20
2012	40	30	221	35	30	192	2	42	0	54	0	0	8	0	2	14
2013	28	15	121	16	15	90	4	48	5	55	0	1	8	1	0	20
Tota	**147**	**110**	**745**	**118**	**106**	**766**	**10**	**131**	**9**	**182**	**0**	**4**	**63**	**2**	**3**	**162**

Table S4. Survival (*S*) sub-model selection results from analysis of mark-recapture-recovery data from the Baffin Bay polar bear subpopulation, 1993–2013. COY = cubs of the year. YRL = yearlings. 2+ = bears aged 2 and older. Age classes separated by a comma were estimated independently; classes not separated by a comma were pooled for estimation. Epoch = periods defined by sampling method (1993–1997, 1998–2010, and 2011–2013). Preliminary analyses suggested that QAIC*c* scores of structures including sea-ice metrics were critically dependent on 1996, the year in which there was no live recapture sampling, which also happened to coincide with heavy sea ice. Structures with sea-ice covariates thus were eliminated from further consideration

***S* sub-model structure**	**Parameters**	**ΔQAICc**	**QAICc weights**	**QDeviance**
COY YRL, 2+(sex × epoch)	22	0.00	0.978	3878.0
COY YRL, 2+(sex + epoch)	20	8.36	0.015	3890.4
COY YRL, 2+(sex)	18	9.83	0.007	3896.0

Table S5. Recapture probability (p) sub-model selection results from analysis of mark-recapture-recovery data from the Baffin Bay polar bear subpopulation, 1993–2013. Family = females / dependent bears and independent males (2 age / sex classes); ice = spring transition date; epoch = sampling period (1993–1995, 1997; 2011–2013); t = full time variation; and inland = proximity of individual's first capture location to smoothed coastline (2 km threshold; binary). All p structures incorporated the radio collar covariate representing bears that were outfitted with collars that may have been used to locate them

***p* sub-model structure**	**Parameters**	**ΔQAICc**	**QAICc weights**	**QDeviance**
family + t	22	0	0.418	3878.0
family + t + coastline (2010s)	23	1.31	0.217	3877.3
family + t + coastline (epoch)	24	1.32	0.216	3875.2
family + epoch + ice	19	3.50	0.073	3887.6
family + epoch + ice + coastline (epoch)	21	4.78	0.038	3884.8
family + epoch + ice + coastline (2010s)	20	4.78	0.038	3886.8
family + epoch	18	15.49	0.0002	3901.6
family + epoch + coastline (2010s)	19	16.96	0.0001	3901.0
family + epoch + coastline (epoch)	20	17.08	0.0001	3899.1
family × epoch	19	17.31	0.0001	3901.4
family × epoch + coastline (epoch)	21	18.66	<0.0001	3898.7
family × epoch + coastline (2010s)	20	18.71	<0.0001	3900.8

Table S6. Fidelity (*F*) sub-model selection results from analysis of mark-recapture-recovery data from the Baffin Bay polar bear subpopulation, 1993–2013. Coy = cubs of the year. Yrl = yearlings. 2+ = bears aged 2 and older. Age classes separated by a comma were estimated independently; classes not separated by a comma were pooled for estimation

***F* sub-model structure**	**Parameters**	**ΔQAICc**	**QAICc weights**	**QDeviance**
Constant	21	0.00	0.57	3878.4
coy yrl 2+ F, 2+ M	22	1.62	0.25	3878.0
Fixed = 1	20	2.28	0.18	3882.7

Table S7. Model selection results (< 4 $\Delta QAIC_c$) from analysis of geographic subset of mark-recapture-recovery data from the Baffin Bay polar bear subpopulation, 1993–2013. COY = cubs of the year. YRL = yearlings. 2+ = bears aged 2 and older. Age classes separated by a comma were estimated independently; classes not separated by a comma were pooled for estimation. For S, epoch = periods defined by sampling method (1993–1997, 1998–2010, and 2011–2013). For p, family = females / dependent bears and independent males (2 age / sex classes); ice = spring transition date; epoch = sampling period (1993–1995, 1997; 2011–2013); inland = proximity of initial capture to smoothed coastline; and t = full time variation. For r, time = 1992–2005 and 2006–2013. All p structures incorporated the radio collar covariate for bears that were outfitted with collars that may have been used to locate them

Model Structures				**Parameters**	**ΔQAICc**	**QAICc weights**	**QDeviance**
S	*P*	*r*	*F*				
COY YRL, 2+(sex × epoch)	family + t	COY, YRL, 2+ (sex + time)	Constant	21	0.00	0.29	3361.5
COY YRL, 2+(sex × epoch)	family + epoch + ice + coastline	COY, YRL, 2+ (sex + time)	Constant	20	0.80	0.19	3364.3
COY YRL, 2+(sex × epoch)	family + epoch + ice	COY, YRL, 2+ (sex + time)	Constant	18	1.09	0.17	3368.7
COY YRL, 2+(sex × epoch)	family + t	COY, YRL, 2+ (sex + time)	COY YRL 3+ F, 3+ M	22	1.71	0.12	3361.2
COY YRL, 2+(sex × epoch)	family + t	COY, YRL, 2+ (sex + time)	Fixed = 1	20	2.46	0.08	3366.0
COY YRL, 2+(sex × epoch)	family + epoch + ice + coastline	COY, YRL, 2+ (sex + time)	COY YRL 3+ F, 3+ M	21	2.49	0.08	3364.0
COY YRL, 2+(sex × epoch)	family + epoch + ice	COY, YRL, 2+ (sex + time)	COY YRL 3+ F, 3+ M	19	2.76	0.07	3368.3

Table S8. Model averaged (<4Δ $QAIC_c$) parameter estimates obtained from mark-recapture study of polar bears in the Baffin Bay subpopulation, 1993–2013, using the geographic data subset

Parameter	Class	Estimate (SE)
Survival (total)	Cubs of the year / yearlings	0.89 (0.06)
	2+ Females, 1990s	0.85 (0.04)
	2+ Females, Gap	0.95 (0.02)
	2+ Females, 2011 – 2013	0.91 (0.05)
	2+ Males, 1990s	0.89 (0.03)
	2+ Males, Gap	0.87 (0.02)
	2+ Males, 2011 – 2013	0.78 (0.06)
Reporting	Cubs of the year	0.08 (0.07)
	Yearlings	0.10 (0.07)
	2+ Females, 1993 – 2005	0.19 (0.05)
	2+ Females, 2006 - 2013	0.17 (0.06)
	2+ Males, 1993 – 2005	0.29 (0.03)
	2+ Males, 2006 – 2013	0.27 (0.06)
Fidelity	Cubs of the year, yearlings, and 2+ females	0.95 (0.03)
	2+ Males	0.95 (0.03)